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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/808,031ADATE: 05/06/1999
TIME: 08:25:11

INPUT SET: S31745.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

 #30

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori

(ii) TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE

(iii) NUMBER OF SEQUENCES: 52

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: WEISER & ASSOCIATES
(B) STREET: 230 South Fifteenth Street, Suite 500
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/808,031
(B) FILING DATE: 03-MAR-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Weiser, Gerard J.
(B) REGISTRATION NUMBER: 19,763
(C) REFERENCE/DOCKET NUMBER: 377(913).5888P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 215-875-8383
(B) TELEFAX: 215-875-8394

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2176 base pairs

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/808,031ADATE: 05/06/1999
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47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: double
49 (D) TOPOLOGY: linear
50
51 (ii) MOLECULE TYPE: cDNA
52
53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 640..2094
57
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG 60
62
63 TGTACCGCGT TTCCCTGGAT GGTACACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT 120
64
65 CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG 180
66
67 CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCCTCGGCA TTGGTCTAAA 240
68
69 CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG 300
70
71 ACGACGTGCG CTTACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC 360
72
73 CTCGAGCGGC GGAGCGGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG 420
74
75 TAGCCTGTTC TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGGTA GCGGAGCCAA 480
76
77 CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG 540
78
79 CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT 600
80
81 GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG 654
82 Met Thr Ala Arg Leu
83 1 5
84
85 GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG 702
86 Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu
87 10 15 20
88
89 CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG 750
90 Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg Glu Ala Arg Arg
91 25 30 35
92
93 CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG 798
94 Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala
95 40 45 50
96
97 GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC 846
98 Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu
99 55 60 65

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/808,031A

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153	ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CGG GAG GCG GTC CAG	1518
154	Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln	
155	280 285 290	
156		
157	TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC	1566
158	Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro	
159	295 300 305	
160		
161	CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG	1614
162	Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys	
163	310 315 320 325	
164		
165	CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC	1662
166	Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr	
167	330 335 340	
168		
169	ACG CGC TAC GCG GAC GAC CTG ACC TTC TCC TGG ACG AAG GCG AAG CAG	1710
170	Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln	
171	345 350 355	
172		
173	CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT	1758
174	Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser	
175	360 365 370	
176		
177	CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC	1806
178	Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp	
179	375 380 385	
180		
181	AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC	1854
182	Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu	
183	390 395 400 405	
184		
185	GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC	1902
186	Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg	
187	410 415 420	
188		
189	GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC	1950
190	Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly	
191	425 430 435	
192		
193	AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC	1998
194	Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala	
195	440 445 450	
196		
197	GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT	2046
198	Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala	
199	455 460 465	
200		
201	CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG	2094
202	Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu	
203	470 475 480 485	
204		
205	TGACGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCCG CATTAGCAA	2154

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206

CTCCGTCAGC CGGCGCGGGT AC

2176

207

208

209

210

(2) INFORMATION FOR SEQ ID NO:2:

211

212

(i) SEQUENCE CHARACTERISTICS:

213

(A) LENGTH: 485 amino acids

214

(B) TYPE: amino acid

215

(D) TOPOLOGY: linear

216

217

(ii) MOLECULE TYPE: protein

218

219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

220

221

Met Thr Ala Arg Leu Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala

222

1

5

10

15

223

224

Val Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys

225

20

25

30

226

227

Arg Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys

228

35

40

45

229

230

Ala Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu

231

50

55

60

232

233

Val Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser

234

65

70

75

80

235

236

Glu Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr

237

85

90

95

238

239

Glu Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr

240

100

105

110

241

242

His Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu

243

115

120

125

244

245

Ala Asp Ala Phe Asp Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn

246

130

135

140

247

248

Gly Leu Thr Glu Leu Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly

249

145

150

155

160

250

251

Leu Ser Val Ser Lys Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp

252

165

170

175

253

254

Thr Ala Thr His Tyr Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser

255

180

185

190

256

257

Lys Arg Thr Ile Thr Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg

258

195

200

205

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